

1643

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/580,201A
 DATE: 11/07/2000
 TIME: 15:56:31

Input Set : A:\2314-187.app
 Output Set: N:\CRF3\11072000\I580201A.raw

ENTERED

3 <110> APPLICANT: McIntosh, J. Michael
 4 Olivera, Baldomero M.
 5 Cruz, Lourdes J.
 6 Corpuz, Gloria P.
 7 Jones, Robert M.
 8 Garrett, James E.
 10 <120> TITLE OF INVENTION: Conotoxin Peptides
 12 <130> FILE REFERENCE: Conotoxin Peptides
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/580,201A
 C--> 15 <141> CURRENT FILING DATE: 2000-05-26
 17 <150> PRIOR APPLICATION NUMBER: US 60/173,298
 18 <151> PRIOR FILING DATE: 1999-12-28
 20 <150> PRIOR APPLICATION NUMBER: US 60/118,381
 21 <151> PRIOR FILING DATE: 1999-01-29
 23 <150> PRIOR APPLICATION NUMBER: US 09/493,143
 24 <151> PRIOR FILING DATE: 2000-01-28
 26 <160> NUMBER OF SEQ ID NOS: 20
 28 <170> SOFTWARE: PatentIn Ver. 2.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 14
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Artificial Sequence
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Description of Artificial Sequence:generic
 37 conotoxin peptide sequence
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 40 <221> NAME/KEY: PEPTIDE
 41 <222> LOCATION: (1)..(2)
 42 <223> OTHER INFORMATION: Xaa at residue 1 is des-Xaa, Asn, Gln or pyro-Glu;
 43 Xaa at residue 2 is des-Xaa, Gly, Ala, Glu, gamma-
 44 carboxy-Glu, Asp, Asn, Ser, Thr, g-Asn (where g is
 45 glycosylation), g-Ser or g-Thr;
 47 <220> FEATURE:
 48 <221> NAME/KEY: PEPTIDE
 49 <222> LOCATION: (3)..(7)
 50 <223> OTHER INFORMATION: Xaa at residue 3 is Val, Ala, Gly, Leu, Ile, Ser,
 51 Thr, g-Asn, g-Ser or g-Thr; Xaa at residue 7 is
 52 Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 53 mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
 W--> 54 O-phospho-Tyr,
 56 <220> FEATURE:
 57 <221> NAME/KEY: PEPTIDE
 58 <222> LOCATION: (7)
 59 <223> OTHER INFORMATION: nitro-Tyr, Trp (D or L), neo-Trp, halo-Trp (D or
 60 L), any synthetic aromatic amino acid, an
 61 aliphatic amino acid bearing linear or branched
 62 saturated hydrocarbon chains such as Leu (D or L),

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W--> 63      Ile and
        65 <220> FEATURE:
        66 <221> NAME/KEY: PEPTIDE
        67 <222> LOCATION: (7)..(8)
        68 <223> OTHER INFORMATION: Val or non-natural derivatives of the aliphatic
        69 amino acid; Xaa at residue 8 is Lys, Arg,
        70 homolysine, homoarginine, ornithine, nor-Lys, His,
        71 N-methyl-Lys, N,N'-dimethyl-Lys,
W--> 72      N,N',N''-trimethyl-Lys,
        74 <220> FEATURE:
        75 <221> NAME/KEY: PEPTIDE
        76 <222> LOCATION: (8)..(9)
        77 <223> OTHER INFORMATION: any synthetic basic amino acid, Ser, Thr, g-Ser,
        78 g-Thr or any hydroxylated synthetic residue; Xaa
        79 at residue 9 is an aliphatic amino acids bearing
        80 linear or branched saturated hydrocarbon chains
W--> 81      such
        83 <220> FEATURE:
        84 <221> NAME/KEY: PEPTIDE
        85 <222> LOCATION: (9)
        86 <223> OTHER INFORMATION: as Leu (D or L), Ile and Val or non-natural
        87 derivatives of the aliphatic amino acid; Met, Phe,
        88 Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr,
        89 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
W--> 90      nitro-Tyr,
        92 <220> FEATURE:
        93 <221> NAME/KEY: PEPTIDE
        94 <222> LOCATION: (9)..(11)
        95 <223> OTHER INFORMATION: Trp (D or L), neo-Trp, halo-Trp (D or L) or any
        96 synthetic aromatic amino acid; Xaa at residue 11
        97 is His, Ser, Thr, g-Ser, g-Thr, an aliphatic amino
        98 acid bearing linear or branched saturated
        100 <220> FEATURE:
        101 <221> NAME/KEY: NP_BIND
        102 <222> LOCATION: (11)
        103 <223> OTHER INFORMATION: hydrocarbon chains such as Leu (D or L), Ile and
        104 Val, non-natural derivatives of the aliphatic
        105 amino acid, Phe, Tyr, meta-Tyr, ortho-Tyr,
        106 nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
        108 <220> FEATURE:
        109 <221> NAME/KEY: PEPTIDE
        110 <222> LOCATION: (11)..(14)
        111 <223> OTHER INFORMATION: O-phospho-Tyr, nitro-Tyr, Trp (D or L), neo-Trp,
        112 halo-Trp (D or L) or a synthetic aromatic amino
        113 acid; Xaa at residue 12 is Pro, hydroxy- Pro (Hyp)
        114 or g-Hyp; Xaa at residue 14 is des-Xaa, Gly, Ala,
        116 <220> FEATURE:
        117 <221> NAME/KEY: PEPTIDE
        118 <222> LOCATION: (14)

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119 <223> OTHER INFORMATION: Lys, Arg, homolysine, homoarginine, ornithine,
120 nor-Lys, His, N-methyl-Lys, N,N'-dimethyl-Lys,
121 N,N',N''-trimethyl-Lys or any synthetic basic
122 amino acid.
124 <400> SEQUENCE: 1
W--> 125 Xaa Xaa Xaa Cys Cys Gly Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa
126 1 5 10
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 13
131 <212> TYPE: PRT
132 <213> ORGANISM: Conus marmoreus
134 <220> FEATURE:
135 <221> NAME/KEY: PEPTIDE
136 <222> LOCATION: (7)..(8)
137 <223> OTHER INFORMATION: Xaa at residue 7 is Tyr, mono-halo-Tyr,
138 di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
139 nitro-Tyr; Xaa at residue 8 is Lys, N-methyl-Lys,
140 N,N-dimethyl-Lys or N,N,N-trimethyl Lys
142 <220> FEATURE:
143 <221> NAME/KEY: PEPTIDE
144 <222> LOCATION: (12)
145 <223> OTHER INFORMATION: Xaa at residue 12 is Pro or hydroxy-Pro.
147 <400> SEQUENCE: 2
W--> 148 Asn Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
149 1 5 10
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 12
154 <212> TYPE: PRT
155 <213> ORGANISM: Conus marmoreus
157 <220> FEATURE:
158 <221> NAME/KEY: PEPTIDE
159 <222> LOCATION: (6)..(7)
160 <223> OTHER INFORMATION: Xaa at residue 6 is Tyr, mono-halo-Tyr,
161 di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
162 nitro-Tyr; Xaa at residue 7 is Lys, N-methyl-Lys,
163 N,N-dimethyl-Lys or N,N,N-trimethyl Lys
165 <220> FEATURE:
166 <221> NAME/KEY: PEPTIDE
167 <222> LOCATION: (11)
168 <223> OTHER INFORMATION: Xaa at residue 11 is Pro or hydroxy-Pro
170 <400> SEQUENCE: 3
W--> 171 Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
172 1 5 10
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 12
177 <212> TYPE: PRT
178 <213> ORGANISM: Unknown
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Unknown Organism: unknown Conus

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182     species
184 <220> FEATURE:
185 <221> NAME/KEY: PEPTIDE
186 <222> LOCATION: (6)..(7)
187 <223> OTHER INFORMATION: Xaa at residue 6 is Tyr, mono-halo-Tyr,
188     di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
189     nitro-Tyr; Xaa at residue 7 is Lys, N-methyl-Lys,
190     N,N-dimethyl-Lys or N,N,N-trimethyl Lys.
192 <220> FEATURE:
193 <221> NAME/KEY: PEPTIDE
194 <222> LOCATION: (11)
195 <223> OTHER INFORMATION: Xaa at residue 11 is Pro or hydroxy-Pro
197 <400> SEQUENCE: 4
W--> 198 Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
      199   1         5             10
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 11
204 <212> TYPE: PRT
205 <213> ORGANISM: Conus bandanus
207 <220> FEATURE:
208 <221> NAME/KEY: PEPTIDE
209 <222> LOCATION: (5)..(6)
210 <223> OTHER INFORMATION: Xaa at residue 5 is Tyr, mono-halo-Tyr,
211     di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
212     nitro-Tyr; Xaa at residue 6 is Lys, N-methyl-Lys,
213     N,N-dimethyl-Lys or N,N,N-trimethyl-Lys;
215 <220> FEATURE:
216 <221> NAME/KEY: PEPTIDE
217 <222> LOCATION: (10)
218 <223> OTHER INFORMATION: Xaa at residue 10 is Pro or hydroxy-Pro (Hyp)
220 <400> SEQUENCE: 5
W--> 221 Ala Cys Cys Gly Xaa Xaa Lys Cys Ser Xaa Cys
      222   1         5             10
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 13
227 <212> TYPE: PRT
228 <213> ORGANISM: Conus textile
230 <220> FEATURE:
231 <221> NAME/KEY: PEPTIDE
232 <222> LOCATION: (1)..(11)
233 <223> OTHER INFORMATION: Xaa at residue 1 is Gln or pyro-Glu; Xaa at
234     residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr,
235     O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr; Xaa at
236     residue 11 is Pro or hydroxy-Pro (Hyp)
238 <400> SEQUENCE: 6
W--> 239 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys Gly
      240   1         5             10
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 13

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Input Set : A:\2314-187.app
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245 <212> TYPE: PRT
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248 <220> FEATURE:
249 <221> NAME/KEY: PEPTIDE
250 <222> LOCATION: (7)..(11)
251 <223> OTHER INFORMATION: Xaa at residue 7 is Lys, N-methy-Lys,
252     N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at
253     residue 11 is Pro or hydroxy-Pro (Hyp)
255 <400> SEQUENCE: 7
W--> 256 Ser Thr Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Arg
      257   1           5           10
260 <210> SEQ ID NO: 8
261 <211> LENGTH: 25
262 <212> TYPE: DNA
263 <213> ORGANISM: Conus marmoreus
265 <220> FEATURE:
266 <221> NAME/KEY: modified_base
267 <222> LOCATION: (14)
268 <223> OTHER INFORMATION: i
270 <400> SEQUENCE: 8
W--> 271 caggatccaa yggngtbtgy tgygg                25
      274 <210> SEQ ID NO: 9
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      276 <212> TYPE: DNA
      277 <213> ORGANISM: Conus marmoreus
      279 <220> FEATURE:
      280 <221> NAME/KEY: modified_base
      281 <222> LOCATION: (26)
      282 <223> OTHER INFORMATION: i
      284 <400> SEQUENCE: 9
W--> 285 ctggatccgg rtgrcavary ttrtancc            28
      288 <210> SEQ ID NO: 10
      289 <211> LENGTH: 23
      290 <212> TYPE: DNA
      291 <213> ORGANISM: Artificial Sequence
      293 <220> FEATURE:
      294 <223> OTHER INFORMATION: Description of Artificial Sequence:universal
      295     primer
      297 <400> SEQUENCE: 10
      298 aagctcgagt aacaacgcag agt                23
      301 <210> SEQ ID NO: 11
      302 <211> LENGTH: 805
      303 <212> TYPE: DNA
      304 <213> ORGANISM: Conus marmoreus
      306 <220> FEATURE:
      307 <221> NAME/KEY: CDS
      308 <222> LOCATION: (82)..(264)
      310 <400> SEQUENCE: 11
      311 ggcgaataca cctggcaggt actcaacgaa cttcaggaca cattcttttc acctggacac 60

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VERIFICATION SUMMARY DATE: 11/07/2000
PATENT APPLICATION: US/09/580,201A TIME: 15:56:32

Input Set : A:\2314-187.app
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L:90 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9